

```

1  AAGTAAAAGAAAGAGCGAGAAATCATCGAAATGGATTTCATCTCATCTCTTATCGTTGGC
   -----+-----+-----+-----+-----+-----+-----+ 60
   TTCATTTTCTTTCTCGCTCTTTAGTAGCTTTACCTAAAGTAGAGTAGAGAATAGCAACCG

a  K * K K E R E I I E (M) D F I S S L I V G -
b  S K R K S E K S S K W I S S H L L S L A -
c  V K E R A R N H R N G F H L I S Y R W L -

   TGTGCTCAGGTGTTGTGTGAATCTATGAATATGGCGGAGAGAAGAGGACATAAGACTGAT
61 -----+-----+-----+-----+-----+-----+ 120
   ACACGAGTCCACAACACACTTAGATACTTATACCGCCTCTCTTCTCCTGTATTCTGACTA

a  C A Q V L C E S M N M A E R R G H K T D -
b  V L R C C V N L * I W R R E E D I R L I -
c  C S G V V * I Y E Y G G E K R T * D * S -

   CTTAGACAAGCCATCACTGATCTTGAAACAGCCATCGGTGACTTGAAGGCCATACGTGAT
121 -----+-----+-----+-----+-----+-----+ 180
   GAATCTGTTTCGGTAGTGACTAGAACTTTGTTCGGTAGCCACTGAACTTCCGGTATGCACTA

a  L R Q A I T D L E T A I G D L K A I R D -
b  L D K P S L I L K Q P S V T * R P Y V M -
c  * T S H H * S * N S H R * L E G H T * * -

   GACCTGACTTTACGGATCCAACAAGACGGTCTAGAGGGACGAAGCTGCTCAAATCGTGCC
181 -----+-----+-----+-----+-----+-----+ 240
   CTGGACTGAAATGCCTAGGTTGTTCTGCCAGATCTCCCTGCTTCGACGAGTTTAGCACGG

a  D L T L R I Q Q D G L E G R S C S N R A -
b  T * L Y G S N K T V * R D E A A Q I V P -
c  P D F T D P T R R S R G T K L L K S C Q -

   AGAGAGTGGCTTAGTGCGGTGCAAGTAACGGAGACTAAAACAGCCCTACTTTTAGTGAGG
241 -----+-----+-----+-----+-----+-----+ 300
   TCTCTCACCGAATCACGCCACGTTTCATTGCCTCTGATTTTGTCTGGGATGAAAATCACTCC

a  R E W L S A V Q V T E T K T A L L L V R -
b  E S G L V R C K * R R L K Q P Y F * * G -
c  R V A * C G A S N G D * N S P T F S E V -

   TTTAGGCGTCGGGAACAGAGGACGCGAATGAGGAGGAGATACCTCAGTTGTTTCGGTTGT
301 -----+-----+-----+-----+-----+-----+ 360
   AAATCCGCAGCCCTTGTCTCCTGCGCTTACTCCTCCTCTATGGAGTCAACAAAGCCAACA

a  F R R R E Q R T R M R R R Y L S C F G C -
b  L G V G N R G R E * G G D T S V V S V V -
c  * A S G T E D A N E E E I P Q L F R L C -

   GCCGACTACAACTGTGCAAGAAGGTTTCTGCCATATTGAAGAGCATTGGTGAGCTGAGA
361 -----+-----+-----+-----+-----+-----+ 420
   CGGCTGATGTTTGACACGTTCTTCAAAGACGGTATAACTTCTCGTAACCACTCGACTCT

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Fig. 2A

Title: RPS GENE FAMILY, PRIMERS, PROBES, AND  
DETECTION METHODS

Applicant(s): Ausubel et al.

Filing Date: July 2, 2003

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Serial No.: Unknown

Customer No.: 21559

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a  A D Y K L C K K V S A I L K S I G E L R -
b  P T T N C A R R F L P Y * R A L V S * E -
c  R L Q T V Q E G F C H I E E H W * A E R -

GAACGCTCTGAAGCTATCAAAACAGATGGCGGGTCAATTCAAGTAACTTGTAGAGAGATA
421 -----+-----+-----+-----+-----+-----+ 480
CTTGCGAGACTTCGATAGTTTTGTCTACCGCCCAGTTAAGTTCATTGAACATCTCTCTAT

a  E R S E A I K T D G G S I Q V T C R E I -
b  N A L K L S K Q M A G Q F K * L V E R Y -
c  T L * S Y Q N R W R V N S S N L * R D T -

CCCATCAAGTCCGTTGTCGGAAATACCACGATGATGGAACAGGTTTTGGAATTTCTCAGT
481 -----+-----+-----+-----+-----+ 540
GGGTAGTTCAGGCAACAGCCTTTATGGTGCTACTACCTTGTCAAAACCTTAAAGAGTCA

a  P I K S V V G N T T M M E Q V L E F L S -
b  P S S P L S E I P R * W N R F W N F S V -
c  H Q V R C R K Y H D D G T G F G I S Q * -

GAAGAAGAAGAAAGAGGAATCATTGGTGTTTATGGACCTGGTGGGGTTGGGAAGACAACG
541 -----+-----+-----+-----+-----+ 600
CTTCTTCTTCTTTCTCCTTAGTAACCACAAATACCTGGACCACCCCAACCCTTCTGTTGC

a  E E E E R G I I G V Y G P G G V G K T T -
b  K K K K E E S L V F M D L V G L G R Q R -
c  R R R K R N H W C L W T W W G W E D N V -

TTAATGCAGAGCATTAAACAACGAGCTGATCACAAAAGGACATCAGTATGATGTACTGATT
601 -----+-----+-----+-----+-----+ 660
AATTACGTCTCGTAATTGTTGCTCGACTAGTGTTTTCTGTAGTCATACTACATGACTAA

a  L M Q S I N N E L I T K G H Q Y D V L I -
b  * C R A L T T S * S Q K D I S M M Y * F -
c  N A E H * Q R A D H K R T S V * C T D L -

TGGGTTCAAATGTCCAGAGAATTCGGCGAGTGTACAATTCAGCAAGCCGTTGGAGCACGG
661 -----+-----+-----+-----+-----+ 720
ACCCAAGTTTACAGGTCTCTTAAGCCGCTCACATGTTAAGTCGTTCCGGCAACCTCGTGCC

a  W V Q M S R E F G E C T I Q Q A V G A R -
b  G F K C P E N S A S V Q F S K P L E H G -
c  G S N V Q R I R R V Y N S A S R W S T V -

TTGGGTTTATCTTGGGACGAGAAGGAGACCGGCGAAAACAGAGCTTTGAAGATATACAGA
721 -----+-----+-----+-----+-----+ 780
AACCCAAATAGAACCCTGCTCTTCCTCTGGCCGCTTTTGTCTCGAAACTTCTATATGTCT

a  L G L S W D E K E T G E N R A L K I Y R -
b  W V Y L G T R R R P A K T E L * R Y T E -
c  G F I L G R E G D R R K Q S F E D I Q S -

GCTTTGAGACAGAAACGTTTCTTGTTGTTGCTAGATGATGTCTGGGAAGAGATAGACTTG
781 -----+-----+-----+-----+-----+ 840
CGAAACTCTGTCTTTGCAAAGAACAACAACGATCTACTACAGACCCTTCTCTATCTGAAC
```

Fig. 2B

```

a  A L R Q K R F L L L L D D V W E E I D L -
b  L * D R N V S C C C * M M S G K R * T W -
c  F E T E T F L V V A R * C L G R D R L G -

      GAGAAACTGGAGTTCCTCGACCTGACAGGGAAAACAAATGCAAGGTGATGTTACGACA
841 -----+-----+-----+-----+-----+-----+ 900
      CTCTTTTGACCTCAAGGAGCTGGACTGTCCCTTTTGTTTACGTTCCACTACAAGTGCTGT

a  E K T G V P R P D R E N K C K V M F T T -
b  R K L E F L D L T G K T N A R * C S R H -
c  E N W S S S T * Q G K Q M Q G D V H D T -

      CGGTCTATAGCATTATGCAACAATATGGGTGCGGAATACAAGTTGAGAGTGGAGTTTCTG
901 -----+-----+-----+-----+-----+-----+ 960
      GCCAGATATCGTAATACGTTGTTATACCCACGCCTTATGTTCAACTCTCACCTCAAAGAC

a  R S I A L C N N M G A E Y K L R V E F L -
b  G L * H Y A T I W V R N T S * E W S F W -
c  V Y S I M Q Q Y G C G I Q V E S G V S G -

      GAGAAGAAACACGCGTGGGAGCTGTTCTGTAGTAAGGTATGGAGAAAAGATCTTTTAGAG
961 -----+-----+-----+-----+-----+-----+ 1020
      CTCTTCTTTGTGCGCACCCCTCGACAAGACATCATTCCATACCTCTTTTCTAGAAAATCTC

a  E K K H A W E L F C S K V W R K D L L E -
b  R R N T R G S C S V V R Y G E K I F * S -
c  E E T R V G A V L * * G M E K R S F R V -

      TCATCATCAATTGCGCGGCTCGCGGAGATTATAGTGAGTAAATGTGGAGGATTGCCACTA
1021 -----+-----+-----+-----+-----+-----+ 1080
      AGTAGTAGTTAAGCGGCCGAGCGCCTCTAATATCACTCATTTACACCTCCTAACGGTGAT

a  S S S I R R L A E I I V S K C G G L P L -
b  H H Q F A G S R R L * * V N V E D C H * -
c  I I N S P A R G D Y S E * M W R I A T S -

      GCGTTGATCACTTTAGGAGGAGCCATGGCTCATAGAGAGACAGAAGAAGAGTGGATCCAT
1081 -----+-----+-----+-----+-----+-----+ 1140
      CGCAACTAGTGAAATCCTCCTCGGTACCGAGTATCTCTCTGTCTTCTTCTCACCTAGGTA

a  A L I T L G G A M A H R E T E E E W I H -
b  R * S L * E E P W L I E R Q K K S G S M -
c  V D H F R R S H G S * R D R R R V D P C -

      GCTAGTGAAGTTCTGACTAGATTTCAGCAGAGATGAAGGGTATGAACTATGTATTTGCC
1141 -----+-----+-----+-----+-----+-----+ 1200
      CGATCACTTCAAGACTGATCTAAAGGTGCTCTCTACTTCCCATACTTGATACATAAACGG

a  A S E V L T R F P A E M K G M N Y V F A -
b  L V K F * L D F Q Q R * R V * T M Y L P -
c  * * S S D * I S S R D E G Y E L C I C P -

      CTTTGTAAATTCAGCTACGACAACCTCGAGAGTGATCTGCTTCGGTCTTGTTTCTTGTA
1201 -----+-----+-----+-----+-----+-----+ 1260
      GAAACTTTAAGTCGATGCTGTTGGAGCTCTCACTAGACGAAGCCAGAACAAGAACATG

```

Fig. 2C

```

a L L K F S Y D N L E S D L L R S C F L Y -
b F * N S A T T T S R V I C F G L V S C T -
c F E I Q L R Q P R E * S A S V L F L V L -

TGCGCTTTATTCCCAGAAGAACATTCTATAGAGATCGAGCAGCTTGTTGAGTACTGGGTC
1261 -----+-----+-----+-----+-----+-----+ 1320
ACGCGAAATAAGGGTCTTCTTGTAAGATATCTCTAGCTCGTCGAACAACTCATGACCCAG

a C A L F P E E H S I E I E Q L V E Y W V -
b A L Y S Q K N I L * R S S S L L S T G S -
c R F I P R R T F Y R D R A A C * V L G R -

GGCGAAGGGTTTCTCACCAGCTCCCATGGCGTTAACACCATTACAGGGATATTTTCTC
1321 -----+-----+-----+-----+-----+-----+ 1380
CCGCTTCCCAAAGAGTGGTCGAGGGTACCGCAATTGTGGTAAATGTTCCCTATAAAAGAG

a G E G F L T S S H G V N T I Y K G Y F L -
b A K G F S P A P M A L T P F T R D I F S -
c R R V S H Q L P W R * H H L Q G I F S H -

ATTGGGGATCTGAAAGCGGCATGTTTGTGGAACCGGAGATGAGAAAACACAGGTGAAG
1381 -----+-----+-----+-----+-----+-----+ 1440
TAACCCCTAGACTTTGCGCGTACAAACAACCTTGGCCTCTACTCTTTTGTGTCCACTTC

a I G D L K A A C L L E T G D E K T Q V K -
b L G I * K R H V C W K P E M R K H R * R -
c W G S E S G M F V G N R R * E N T G E D -

ATGCATAATGTGGTCAGAAGCTTTGCATTGTGGATGGCATCTGAACAGGGGACTTATAAG
1441 -----+-----+-----+-----+-----+-----+ 1500
TACGTATTACACCAGTCTTCGAAACGTAACACCTACCGTAGACTTGTCCTCCTGAATATTC

a M H N V V R S F A L W M A S E Q G T Y K -
b C I M W S E A L H C G W H L N R G L I R -
c A * C G Q K L C I V D G I * T G D L * G -

GAGCTGATCCTAGTTGAGCCTAGCATGGGACATACTGAAGCTCCTAAAGCAGAAAACCTGG
1501 -----+-----+-----+-----+-----+-----+ 1560
CTCGACTAGGATCAACTCGGATCGTACCCTGTATGACTTCGAGGATTTTCGTCTTTTGACC

a E L I L V E P S M G H T E A P K A E N W -
b S * S * L S L A W D I L K L L K Q K T G -
c A D P S * A * H G T Y * S S * S R K L A -

CGACAAGCGTTGGTGATCTCATTGTTAGATAACAGAATCCAGACCTTGCCTGAAAACTC
1561 -----+-----+-----+-----+-----+-----+ 1620
GCTGTTCGCAACCACTAGAGTAACAATCTATTGTCTTAGGTCTGGAACGGACTTTTTGAG

a R Q A L V I S L L D N R I Q T L P E K L -
b D K R W * S H C * I T E S R P C L K N S -
c T S V G D L I V R * Q N P D L A * K T H -

```

Fig. 2D



ATATGCCCGAAACTGACAACACTGATGCTCCAACAGAACAGCTCTTTGAAGAAGATTCCA  
1621 -----+-----+-----+-----+-----+-----+ 1680  
TATACGGGCTTTGACTGTTGTGACTACGAGGTTGTCTTGTGCGAGAACTTCTTCTAAGGT

a I C P K L T T L M L Q Q N S S L K K I P -  
b Y A R N \* Q H \* C S N R T A L \* R R F Q -  
c M P E T D N T D A P T E Q L F E E D S N -

ACAGGGTTTTTCATGCATATGCCTGTTCTCAGAGTCTTGGACTTGTCTTCACAAGTATC  
1681 -----+-----+-----+-----+-----+-----+ 1740  
TGTCCTCAAAAAGTACGTATACGGACAAGAGTCTCAGAACCTGAACAGCAAGTGTTTCATAG

a T G F F M H M P V L R V L D L S F T S I -  
b Q G F S C I C L F S E S W T C R S Q V S -  
c R V F H A Y A C S Q S L G L V V H K Y H -

ACTGAGATTCCGTTGTCTATCAAGTATTTGGTGGAGTTGTATCATCTGTCTATGTCAGGA  
1741 -----+-----+-----+-----+-----+-----+ 1800  
TGACTCTAAGGCAACAGATAGTTCATAAACCACCTCAACATAGTAGACAGATACAGTCCT

a T E I P L S I K Y L V E L Y H L S M S G -  
b L R F R C L S S I W W S C I I C L C Q E -  
c \* D S V V Y Q V F G G V V S S V Y V R N -

ACAAAGATAAGTGTATTGCCACAGGAGCTTGGGAATCTTAGAAACTGAAGCATCTGGAC  
1801 -----+-----+-----+-----+-----+-----+ 1860  
TGTTTCTATTACATAACGGTGTCTCGAACCCTTAGAATCTTTTGACTTCGTAGACCTG

a T K I S V L P Q E L G N L R K L K H L D -  
b Q R \* V Y C H R S L G I L E N \* S I W T -  
c K D K C I A T G A W E S \* K T E A S G P -

CTACAAAGAACTCAGTTTCTTCAGACGATCCCACGAGATGCCATATGTTGGCTGAGCAAG  
1861 -----+-----+-----+-----+-----+-----+ 1920  
GATGTTTCTTGAGTCAAAGAAGTCTGCTAGGGTGCTCTACGGTATACAACCGACTCGTTC

a L Q R T Q F L Q T I P R D A I C W L S K -  
b Y K E L S F F R R S H E M P Y V G \* A S -  
c T K N S V S S D D P T R C H M L A E Q A -

CTCGAGGTTCTGAACTTGTACTACAGTTACGCCGGTTGGGAAGTGCAGAGCTTTGGAGAA  
1921 -----+-----+-----+-----+-----+-----+ 1980  
GAGCTCCAAGACTTGAACATGATGTCAATGCGGCCAACCTTGACGTCTCGAAACCTCTT

a L E V L N L Y Y S Y A G W E L Q S F G E -  
b S R F \* T C T T V T P V G N C R A L E K -  
c R G S E L V L Q L R R L G T A E L W R R -

GATGAAGCAGAAGAACTCGGATTCGCTGACTTGGAACTTGGAAAACCTAACCACACTC  
1981 -----+-----+-----+-----+-----+-----+ 2040  
CTACTTCGTCTTCTTGAGCCTAAGCGACTGAACCTTATGAACCTTTTGGATTGGTGTGAG

Fig. 2E

```

a   D E A E E L G F A D L E Y L E N L T T L -
b   M K Q K N S D S L T W N T W K T * P H S -
c   * S R R T R I R * L G I L G K P N H T R -

GGTATCACTGTTCTCTCATTGGAGACCCTAAAACTCTCTTCGAGTTCGGTGCTTTGCAT
2041 -----+-----+-----+-----+-----+-----+ 2100
CCATAGTGACAAGAGAGTAACCTCTGGGATTTTGTAGAGAAGCTCAAGCCACGAAACGTA

a   G I T V L S L E T L K T L F E F G A L H -
b   V S L F S H W R P * K L S S S S V L C I -
c   Y H C S L I G D P K N S L R V R C F A * -

AAACATATACAGCATCTCCACGTTGAAGAGTGCAATGAACTCCTCTACTTCAATCTCCCA
2101 -----+-----+-----+-----+-----+ 2160
TTTGTATATGTCGTAGAGGTGCAACTTCTCACGTTACTTGAGGAGATGAAGTTAGAGGGT

a   K H I Q H L H V E E C N E L L Y F N L P -
b   N I Y S I S T L K S A M N S S T S I S H -
c   T Y T A S P R * R V Q * T P L L Q S P I -

TCACTCACTAACCATGGCAGGAACCTGAGAAGACTTAGCATTAAAAGTTGCCATGACTTG
2161 -----+-----+-----+-----+-----+ 2220
AGTGAGTGATTGGTACCGTCCTTGGACTCTTCTGAATCGTAATTTTCAACGGTACTGAAC

a   S L T N H G R N L R R L S I K S C H D L -
b   H S L T M A G T * E D L A L K V A M T W -
c   T H * P W Q E P E K T * H * K L P * L G -

GAGTACCTGGTCACACCCGCAGATTTTGAAATGATTGGCTTCCGAGTCTAGAGGTTCTG
2221 -----+-----+-----+-----+-----+ 2280
CTCATGGACCAGTGTGGGCGTCTAAACTTTTACTAACCGAAGGCTCAGATCTCCAAGAC

a   E Y L V T P A D F E N D W L P S L E V L -
b   S T W S H P Q I L K M I G F R V * R F * -
c   V P G H T R R F * K * L A S E S R G S D -

ACGTTACACAGCCTTCACAACTTAACCAGAGTGTGGGGAAATTCTGTAAGCCAAGATTGT
2281 -----+-----+-----+-----+-----+ 2340
TGCAATGTGTCCGAAGTGTGAATTGGTCTCACACCCCTTTAAGACATTGGTTCTAACA

a   T L H S L H N L T R V W G N S V S Q D C -
b   R Y T A F T T * P E C G E I L * A K I V -
c   V T Q P S Q L N Q S V G K F C K P R L S -

CTGCGGAATATCCGTTGCATAAACATTTACACTGCAACAAGCTGAAGAATGTCTCATGG
2341 -----+-----+-----+-----+-----+ 2400
GACGCCTTATAGGCAACGTATTTGTAAAGTGTGACGTTGTTGACTTCTTACAGAGTACC

a   L R N I R C I N I S H C N K L K N V S W -
b   C G I S V A * T F H T A T S * R M S H G -
c   A E Y P L H K H F T L Q Q A E E C L M G -

GTTCAGAACTCCCAAAGCTAGAGGTGATTGAACTGTTGACTGCAGAGAGATAGAGGAA
2401 -----+-----+-----+-----+-----+ 2460
CAAGTCTTTGAGGGTTTCGATCTCCAATACTTGACAAGCTGACGTCTCTCTATCTCCTT

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Fig. 2F

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a V Q K L P K L E V I E L F D C R E I E E -
b F R N S Q S * R * L N C S T A E R * R N -
c S E T P K A R G D * T V R L Q R D R G I -

TTGATAAGCGAACACGAGAGTCCATCCGTCGAAGATCCAACATTGTTCCCAAGCCTGAAG
2461 -----+-----+-----+-----+-----+-----+ 2520
AACTATTCGCTTGTGCTCTCAGGTAGGCAGCTTCTAGGTTGTAACAAGGGTTCGGACTTC

a L I S E H E S P S V E D P T L F P S L K -
b * * A N T R V H P S K I Q H C S Q A * R -
c D K R T R E S I R R R S N I V P K P E D -

ACCTTGAGAACTAGGGATCTGCCAGAACTAAACAGCATCCTCCCATCTCGATTTTCATTC
2521 -----+-----+-----+-----+-----+-----+ 2580
TGGAACCTTTGATCCCTAGACGGTCTTGATTTGTCGTAGGAGGGTAGAGCTAAAAGTAAG

a T L R T R D L P E L N S I L P S R F S F -
b P * E L G I C Q N * T A S S H L D F H S -
c L E N * G S A R T K Q H P P I S I F I P -

CAAAAAGTTGAAACATTAGTCATCACAATTGCCCCAGAGTTAAGAACTGCCGTTTCAG
2581 -----+-----+-----+-----+-----+-----+ 2640
GTTTTTCAACTTTGTAATCAGTAGTGTTTAAACGGGGTCTCAATTCTTTGACGGCAAAGTC

a Q K V E T L V I T N C P R V K K L P F Q -
b K K L K H * S S Q I A P E L R N C R F R -
c K S * N I S H H K L P Q S * E T A V S G -

GAGAGGAGGACCCAGATGAACTTGCCAACAGTTTATTGTGAGGAGAAATGGTGGAAGCA
2641 -----+-----+-----+-----+-----+-----+ 2700
CTCTCCTCCTGGGTCTACTTGAACGGTGTCAAATAACACTCCTCTTTACCACCTTTCGT

a E R R T Q M N L P T V Y C E E K W W K A -
b R G G P R * T C Q Q F I V R R N G G K H -
c E E D P D E L A N S L L * G E M V E S T -

CTGGAAAAGATCAACCAAACGAAGAGCTTTGTTATTTACCGCGCTTTGTTCCAAATTGA
2701 -----+-----+-----+-----+-----+-----+ 2760
GACCTTTTTCTAGTTGGTTTGCTTCTCGAAACAATAAATGGCGCGAAACAAGGTTTAACT

a L E K D Q P N E E L C Y L P R F V P N * -
b W K K I N Q T K S F V I Y R A L F Q I D -
c G K R S T K R R A L L F T A L C S K L I -

TATAAGAGCTAAGAGCACTCTGTACAAATATGTCCATTTCATAAGATGCAGGAAGCCAGGA
2761 -----+-----+-----+-----+-----+-----+ 2820
ATATTCTCGATTCTCGTGAGACATGTTTATACAGGTAAGTATTCTACGTCCTTCGGTCCT

a Y K S * E H S V Q I C P F I R C R K P G -
b I R A K S T L Y K Y V H S * D A G S Q E -
c * E L R A L C T N M S I H K M Q E A R K -

AGGTTGTTCCAGTGAAGTCATCAACTTTCCACATAGCCACAAAAGTAGAGATTATGTAAT
2821 -----+-----+-----+-----+-----+-----+ 2880
TCCAACAAGGTCACTTCAGTAGTTGAAAGGTGTATCGGTGTTTGTATCTCTAATACATTA

```

Fig. 2G



a R L F Q \* S H Q L S T \* P Q N \* R L C N -  
b G C S S E V I N F P H S H K T R D Y V I -  
c V V P V K S S T F H I A T K L E I M \* S -

CATAAAAACCAAACCTATCCGCGA  
2881 -----+-----+---- 2903  
GTATTTTGGTTTGATAGGCGCT

a H K N Q T I R -  
b I K T K L S A -  
c \* K P N Y P R -

ENZYMES THAT DO CUT:

NONE

ENZYMES THAT DO NOT CUT:

KpnI

Fig. 2H

-146

ATCGATTGATCTCTGGCTCAGTGCGAGTAGTCCATTTGAGAGCAGTCGTAGCCCCGCGTG -86

GCGCATCATGGAGCTATTTGGAATTTTCGCAGGGTTATCGATTTCGTAGTGGGAACCCATT -26

CATTGTTTGAACCACCAACGGACGACTTAACAAGCTCCCCGAGGTGCATGATGAAAATT 35  
MetLysIle

GCTCCAGTTGCCATAAATCACAGCCCGCTCAGCAGGGAGGTCCCGTCACACGCGGCACCC 95  
AlaProValAlaIleAsnHisSerProLeuSerArgGluValProSerHisAlaAlaPro

ACTCAGGCAAAGCAAACCAACCTTCAATCTGAAGCTGGCGATTTAGATGCAAGAAAAAGT 155  
ThrGlnAlaLysGlnThrAsnLeuGlnSerGluAlaGlyAspLeuAspAlaArgLysSer

AGCGCTTCAAGCCCGGAAACCCGCGCATTACTCGCTACTAAGACAGTACTCGGGAGACAC 215  
SerAlaSerSerProGluThrArgAlaLeuLeuAlaThrLysThrValLeuGlyArgHis

AAGATAGAGGTTCCGGCCTTTGGAGGGTGGTTCAAAAAGAAATCATCTAAGCACGAGACG 275  
LysIleGluValProAlaPheGlyGlyTrpPheLysLysLysSerSerLysHisGluThr

GGCGGTTCAAGTGCCAACGCAGATAGTTTCGAGCGTGGCTTCCGATTCCACCGAAAAACCT 335  
GlyGlySerSerAlaAsnAlaAspSerSerSerValAlaSerAspSerThrGluLysPro

TTGTTCCGTCTCACGCACGTTTCCTTACGTATCCCAAGGTAATGAGCGAATGGGATGTTGG 395  
LeuPheArgLeuThrHisValProTyrValSerGlnGlyAsnGluArgMetGlyCysTrp

TATGCCTGCGCAAGAATGGTTGGCCATTCTGTCTGAAGCTGGGCCTCGCCTAGGGCTGCCG 455  
TyrAlaCysAlaArgMetValGlyHisSerValGluAlaGlyProArgLeuGlyLeuPro

GAGCTCTATGAGGGAAGGGAGGCGCCAGCTGGGCTACAAGATTTTTCAGATGTAGAAAGG 515  
GluLeuTyrGluGlyArgGluAlaProAlaGlyLeuGlnAspPheSerAspValGluArg

TTTATTCACAATGAAGGATTAACCTCGGGTAGACCTTCCAGACAATGAGAGATTTACACAC 575  
PheIleHisAsnGluGlyLeuThrArgValAspLeuProAspAsnGluArgPheThrHis

Fig. 3A

GAAGAGTTGGGTGCACTGTTGTATAAGCACGGGCCGATTATATTTGGGTGGAAACTCCG 635  
GluGluLeuGlyAlaLeuLeuTyrLysHisGlyProIleIlePheGlyTrpLysThrPro

AATGACAGCTGGCACATGTCGGTCCTCACTGGTGTGATAAAGAGACGTCGTCCATTACT 695  
AsnAspSerTrpHisMetSerValLeuThrGlyValAspLysGluThrSerSerIleThr

TTTCACGATCCCCGACAGGGGCCGACCTAGCAATGCCGCTCGATTACTTTAATCAGCGA 755  
PheHisAspProArgGlnGlyProAspLeuAlaMetProLeuAspTyrPheAsnGlnArg

TTGGCATGGCAGGTTCCACACGCAATGCTCTACCGCTAAGTAGCAGGGTATCTTCACGTG 815  
LeuAlaTrpGlnValProHisAlaMetLeuTyrArgEnd

GCGGCATCATGACAAGCCCATGATGCCGCCAGCAGCTACCTGAATGCCGTCTGGCTTTTT 875  
←————→

GGTCCCTATTGTCGTATCCGGAAGATGACGTCAAAGAATCTCGGCAAGAGCTTTCTTGCT 935

CGACTCCTCAGCTTCCGGATCGATCAGGTCGCTTGCCAGAGCGCGCTTGTCATGAGCAT 995

CTGCCACAGCTGCTGGTCGATGGTGTCTCAGCTAAAGGGATTTTGACGACAACCATGCG 1055

CAACTGCCCCGTTGCGATACGCTCGATCCTGAAGCCCCGGTGTCCATGGCAGCCCCAAGAA 1115

AAAGACATAGTTCGCCGCTGTGAGGTTGTAGCCTGTGCCGGCGGCGACCTGGTCCCGAT 1175

AAACACCCTGCAGTCCGGATCCTGCTGGAAAGCATCAATCGCCTTCTGCCGCTTCTTGGG 1235

CGAGTCACTGCCCACCAACGTCACGCACCCGACGCCAAGCTTGAGGCAGTGCTCCCGCAA 1295

CGTGGCCACGGATTCCTGATACTCGCAGAAGAGGATCACCTTGTCGTGAC 1346

Fig. 3B

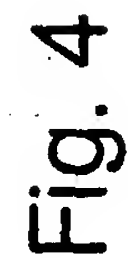


Fig. 4

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	1					50
L6pro	MSYLREVATA	VALLLPFILL	NKFWRPNSKD	SIVNDDDDST	SEVDAISDST	
Nprot	.....	.....	.....	.....	.....	M
PrfP	.....	.....	.....	.....	.....	
rps2	.....	.....	.....	.....	.....	
	51	6				100
L6pro	NPSGSFPSVE	YEVFLSFRGP	DTREQFTDFL	YQSLRRYKIM	TFRDDDELLK	
Nprot	ASSSSSSRWS	YDVFLSFRGE	DTRKTFTSHL	YEVLNKGIK	TFQDDKRLEY	
PrfP	.....	.....	.....	LRSKLDLIID	LKHQIESVKE	
rps2	.....	MDFISSLIVG	CAQVLCESMN	MAERRGHKTD	LRQAITDLET	
	101					150
L6pro	GKEIGPNLLR	AIDQSKIYVP	IISSGYADSK	WCLMELAEIV	RRQEEDPRRI	
Nprot	GATIPGELCK	AIEESQFAIV	VFSENYATSR	WCLNELVKIM	ECK.TRFKQT	
PrfP	GLLCLRSFID	HFSESYDEHD	.....EA	CGLIARVSVM	AYKAE.....	
rps2	AIGDLKAIRD	DLTLRIQQDG	LEGRSCSNRA	REWLSAVQVT	ETKTA.....	
	151	7				200
L6pro	ILPIFYMVDP	SDVRHQTCGY	KKAFRKHANK	F..DGQTIQN	WKDALKKVG	
Nprot	VIPIFYDVDP	SHVRNQKESF	AKAFEEHETK	YKDDVEGIQR	WRIALNEAAN	
PrfP	.....YVIDS	CLAYSHPLWY	KVLW.....	..IS.....	.EVLENIKLV	
rps2	.....LLLVR	FRRREQTRM	RRRY.....	..LSCFGCAD	YKLCKKVS	
	201					8 250
L6pro	LKGWHIGKND	KQGAIADKVS	ADIWSHISKE	NLILE...TD	ELVGIDDHIT	
Nprot	LKGSCDNRDK	TDADCIRQIV	DQISSKLCKI	SLSY...LQ	NIVGIDTHLE	
PrfP	NKVVGETCER	RNIEVTVHEV	AKTTTYVAPS	FSAYTORANE	EMEGFQDTID	
rps2	LKSIGELRER	SEAIKTDGGS	IQVTCREIPI	KSVVG.....	.....NTTMM	
	251		1	-P-loop		300
L6pro	AVLEKLSLDS	ENVTMVGLYG	MGGIGKTTTA	KAVYNKI...	..SSC.FDCC	
Nprot	KIESLLEIGI	NGVRIMGIWG	MGGVGKTTIA	RAIFDTLLGR	MDSSYQFDGA	
PrfP	ELKDKLLGGS	PELDVISIVG	MPGLGKTTLA	KKIYNDPEVT	..SRFDVHAQ	
rps2	EQVLEFLSEE	EERGIIGVYG	PGGVGKTTLM	QSINNELITK	..G....HQY	
	301					350
L6pro	CFIDNIRETQ	EKDGVVVLQK	KLVSEILRID	..SGSVGFNN	DSGGRKTIKE	
Nprot	CFLKDIKE..	NKRGMHSLQN	ALLSELLR..	...EKANYNN	EEDGKHQMAS	
PrfP	CVVTQLYSWR	EL.LLTILND	VLEP...S..	...DRNEKED	GE.IADELRR	
rps2	DVLIWVQMSR	EF.GECTIQQ	AVGA...RLG	..LSWDEKET	GENRALKIYR	
	351	2		3		400
L6pro	RVSRLFILVV	LDDVDEKFKF	EDMLGSPKDF	ISQ.SRFIIT	SRSMRVLGTL	
Nprot	RLRSKKVLIV	LDDIDNKDHY	LEYLAGDLDW	FGNGSRIIIT	TRDKHLI...	
PrfP	FLLTKRFLIL	IDDVWDYKVV	DNLCMCFSD.	VSNRSRIILT	TRLNDVAEYV	
rps2	ALRQKRFLLL	LDDVWEEIDL	EKTGVPRPD.	RENKCKVMFT	TRSIALCNM	

Fig. 5A-1



	401		450
L6pro	NEN.QCKLYE VGSMKPRSL ELFSKHAFKK NT....PPSY YETLANDVVD		
Nprot	.EK.NDIIYE VTALPDHESI QLFKQHAFGK EV....PNEN FEKLSLEVVN		
PrfP	.KC.ESDPHH LRLFRDDES TLLQKEVFQG E....SCPPE LEDVGFEISK		
rps2	.GA.EYK.LR VEFLEKKHAW ELFCSKVWRK DLLESSSIRR LAEI...IVS		
	451	4	500
L6pro	TTAGLPLTLK VIGSLLFKQE IAV..WEDTL EQL....RRT LNLDEVYDRL		
Nprot	YAKGLPLALK VWGSLHNLRL LTE..WKSAL EHM....KNN .SYSGIIDNV		
PrfP	SCRGLPLSVV LVAGVLKQKK KTLD SWKVVE QSL..SQRI GSLEESISII		
rps2	KCGGLPLALI TLGGAMAH.R ETEEWIHAS EVLTRFPAEM KGMNYVFALL		
	501	5	550
L6pro	KISYDALNPE .AKEIFLDIA CFFIGQ..NK EEPYMWTDN NFYPASNIIF		
Nprot	KISYDGLPEK .QQEMFLDIA CFLRGE..EK DYILQILESC HIGAEYGLRI		
PrfP	GFSYKNL.PH YLKPCFLYFG GFLQKDIHD SKMTKLWVAE EFVQANN...		
rps2	KFSYDNLESD LLRSCFLYCA LFPEEHSIEI EQLVEYWVGE GFLTSSHGVN		
	551	10	600
L6pro	LIQRCMIQVG .....DD DEFKMHDQLR DMGREIVRRE DVL PWKRSRI		
Nprot	LIDKSLVFIS .....EY NQVOMHDLIQ DMGKYIVNFQ KD.PGERSRL		
PrfP	.....EK GQEDTRTRF. .LGRSYW... ..		
rps2	TIYKGYFLIG DLKAACLLET GDEKTQVKMH NVVRSFALWM ASEQGTYKEL		
	601		650
L6pro	WSAEEGIDLL LNKKGSSKVK AISI.PWGVK YEFK.SECFL NLSELRYLHA		
Nprot	WLAKEVEEVM SNNTGTMAE AIWSSYSST LRFS.NQAVK NMKRLRVFNM		
PrfP	.....		
rps2	ILVEPSMGHT EAPKAENWRQ ALVISLLDNR IQTL.PEKLI CPKLTTLMLQ		
	651		700
L6pro	REAMLTGDFN NLLPNLKWLE LPFYKHGEDD PPLTNYTMKN LII.VILEHS		
Nprot	GRSSTHYAID YLPNNLRFCV CTNYPW...E SFPSTFELKM LVH.LQLRH.		
PrfP	.....		
rps2	QNSSLKKIPT GFFMHMPVLR VLDLSF.... TSITEIPLSI KYL.VELYHL		
	701		750
L6pro	HITADDWGGW RHMMKMAERL KVVRLASNYS LYGRRVR... ..		
Nprot	.....NSL RHLWTETKHL PSL.....RRID... ..		
PrfP	.....		
rps2	SMSGTKISVL PQELGNLRKL KHLDLQRTQF LQTIPRDAIC WLSKLEVLNL		
	751		800
L6pro	.LSD.CWRFP KSIEVLSMTA IEMDEVDIGE LKKLKTLLVK FCPIQKISGG		
Nprot	.LSW.SKRLT RTPDFTGMPN LEY..VNLYQ CSNLEEVHHS LGCCSKVIGL		
PrfP	.....		
rps2	YYSY.AGWEL QSFGEDEAEE LGFADLEYLE NLTTLGITVL SLETLKTLFE		

Fig. 5A-2

	801		850
L6pro	TFGMLKGLRE	L.CLEFNWGT	NLREVVADIG QLSSLKVLKT
Nprot	YLNDCKSLKR	F.....	.....PCVNVESLE
PrfP	.....	.....	.....
rps2	FGALHKHIQH	L.HVEECNEL	LYFNLPSLTN HGRNLRRLSI
	851		900
L6pro	FPLGLK....	...ELSTSSR	IPNLSQLLDL EVLKVYDCKD
Nprot	Y.LGLR....	...SCDSLEK	LPEIYGRMKP EI.....
PrfP	.....	.....	.....
rps2	TPADFENDWL	PSLEVLTLHS	LHNLTRVWGN SVSQDCLRNI
	901		950
L6pro	EDESSVWWKV	SKLKSLEK	TRINNVVDD ASSGGHLPY
Nprot	ELPSSIFQYK	THVTKLL..	.WNMKNLVAL PSSICRL...
PrfP	.....	.....	.....
rps2	LKNVSWVQKL	PKLEVIELFD	CREIEELISE HESPSVEDPT
	951		1000
L6pro	IYQCTEPTWL	P.GIENLENL	TSLEVNDIFQ TLGGDLGLQ
Nprot	VSGCSKLESL	PEEIGDLNL	RVFDASDTL. ....
PrfP	.....	.....	.....
rps2	TRDLPELNSI	LPSRFSFQKV	ETLVITNCPR VKKLPFQERR
	1001		1050
L6pro	RKVNGLARIK	GLKDLLCSST	CKLRKFYITE CPDLIELLPC
Nprot	P.....	.....SSI	IRLNKLIILM FRGFKDGVHF
PrfP	.....	.....	.....
rps2	EEKWWKALEK	DQPNEELCYL	PRFVPN....
	1051		1100
L6pro	SMAELTIRDC	PRLEVGP MIR	SLPKFPMLKK LDLAVANITK
Nprot	SLEYLNL.SY	CNLIDGGLPE	EIGSLSSLKK LDLSRNNF..
PrfP	.....	.....	.....
rps2	.....	.....	.....
	1101		1150
L6pro	EELVSLELEL	DDTSSGIERI	VSSSKLQKLT TLVVKVPSLR
Nprot	GALQSLDLK.	.....	.DCQRLTQLP ELPPELNELH
PrfP	.....	.....	.....
rps2	.....	.....	.....
	1151		1200
L6pro	LQDLYLEGCT	SLGRPLEKL	KE.....LD IGGCPDLTEL
Nprot	IHDL.VTKRK	KLHRVKLDDA	HNDTMYNLFA YTMFQNISSM
PrfP	.....	.....	.....
rps2	.....	.....	.....

Fig. 5A-3

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```
1201                                     1250
L6pro RGLTIRDCPR LEVGPMIQSL PKFPMLNELT LSMVNITKED ELEVLSLEE
Nprot .SLTV..... FTGQPYPEKI PSWFHHQGWD .SSVSVNLPE NWYIPDKFLG
PrfP .....
rps2 .....
```

```
1251                                     1300
L6pro LD.SLELTLD DTCSSIERIS FLSKLQKLTT LIVEVPSLRE IEGLAELKSL
Nprot FAVCYSRSLI DTTAHLIPVC .DDKMSRMTQ KLALSECDTE SSNYSEWD.I
PrfP .....
rps2 .....
```

```
1301                                     1350
L6pro RILYL..... .EGCTSLERL WPDQQQLGSL KNLNVLDIQG
Nprot HFFFVFPFAGL WDTSKANGKT PNDYGIIRLS FSGEKMYGL RLLYKEGPEV
PrfP .....
rps2 .....
```

```
1351                                     1387
L6pro CKSLSDHLS ALKTTLPRA RITWPDQPYR .....
Nprot NALLQMRENS NEPTEHSTGI RRTQYNNRTS FYELING
PrfP .....
rps2 .....
```

Fig. 5A-4

Fig. 5B-1

```

N   539 SSTLRFSNQAVKNMKRLRVFNMGRSSTHYAIDYLPNNLRFCVCTNYPW.. 586
      : .. |...: |:: || :: . ::: | ||: : . |.
L6  591 GVKYEFKSECFLNLSELYLHAREAMLTGDFNNLLPNLKWLELPFYKHGE 640

N   587 .ESFPSTFELKMLVHLQLRH.....NSLRHLWTETKHLPSL..... 621
      :. :...: | |:: : | | :::||: . :...: |. :
L6  641 DDPPLTNYTMKNLIIVILEHSHITADDWGGWRHMMKMAERLKVVRLASNY 690

N   622 ....RRIDLSWSKRLTRTPDFTGMPNLEY..VNLYQCSNLEEVHHSLGCC 665
      ||: || :. |::: . : |::: | ::: : .. |::: :...
L6  691 SLYGRRVRLSDCWRFPKSIEVLSMTAIEMDEVDIGELKKLKTLLVLKFCPI 740

N   666 SKVIGLYLNDCKSLKRFPVNVESLEYLGLRSCDSLEKLPEIYGRMKP.. 713
      |: | :. |::: : : |::: | |::: | |::: | |::: |
L6  741 QKISGGTFGMLKGLREL.....CLEFNWGTNLREVVDIGQLSSLK 781

N   714 .....EIQIHMQSGGIRELP.SSIFQYKTHVTKLLLWNM....KNLV 750
      |::|: . |::||. || :. ::: . | ::: :...
L6  782 VLKTTGAKEVEINEFPLGLKELSTSSRIPNLSQLLDLEVVLKVYDCKDGF 831
      ||
N   751 ALPSSICRLKSLVSLVSGC SKLES LP EEIGDLNLRVFDASDTLILRP. 799
      |. | : . | |::: | |||. | |. : : | |||. |..
L6  832 MPPASPSEDESSVWVKV... SKLKS LQ LEKTRINVNVVDDASSGGHLP 878
      |
N   800 .....PSSIIRLNKLIILMFRGFKDGVHFEFPPVAE 830
      : | . |::|. | ::: : : : : : :
L6  879 LLPTSLTYLKIYQCTEPTWLPGIENLENLTSLEVNDIFQTLGGDLGL.Q 927
      12
N   831 GLHSLEYLNL SYCNLID..GGLPEEI.GSLSSLKKLDL..SRNNFEHLPS 875
      ||: |||. |::: . | :. ||: : : | :::|: : : : | ||:
L6  928 GLRSLEILRIRKVNGLARIKGLKDLLCSSTCKLRKFYITECPDLIELLPC 977

N   876 SIA....QLGALQSLDLKDCQRLTQLPELPPELNELHVDCHMALKFIHYL 921
      ::: :...: |::| |. | :::: .. | ::: | | :...
L6  978 ELGGQTVVVP SMAELTIRDCPRL.EVGPMIRSLPKFPM.....LKKDLA 1021

N   922 VTKRKKLHRVKLDDAHNDTMYNLFAYTMFQNISSMRHDISASDSLSTVF 971
      |...: | . :. : : : : : : : : |::: : : |. |. | |::
L6  1022 VANITKEEDLDAIGSLEELV..SLELELDDTSSGIERIVSSSKLQKLTL 1069

N   972 TGQPYPEKIPSWFHHQGWDSVSVN.....LPENWYIPDKFLGFAVCY 1014
      .. |::|: . : |::: |: . :. : |: :...
L6  1070 VV.....KVPSLREIEGLEELKSLQDLYLEGCTSLGRLPLEKLELDIGG 1114

```

Fig. 5B-2



**Fig. 5B-3**

-32 ACAAGTAAAGAAAGAGCGGAGAAATCATCGAA -1

ATGATTTTCATCTCATCTTATTCGTTGGCTGTGCTCAGGTGTTGTGATCTATGATATGCGGAGAGAGAGACATAGACTGATCTTAGACAAGCCATCAGTCTTGAACA  
M D F I S S L I V G C A Q V L C E S M N M A E R R G H K T D L R Q A I T D L E T 120  
40  
relatively hydrophobic

GCCATCGTGAAGGCCATACGTGATGACCTGACTTTACGGATCCACAGACGGTTTAGAGGAGCGAAGCTGCTCAATCTGCCAGAGAGTGGCTTAGTGGGTCAGTAACG  
A I G D L K A I R D D L T L R I Q Q D G L E G R S C S N R A R E W L S A V Q V T 240  
80  
leucine-zipper

GAGACTAAACAGCCCTACTTTTACTGAGCTTTAGCGCTCGGACAGAGAGACCGAATGACGAGAGATACCTCAGTTGTTCCGTTGTGCCACTACAACGTGCAAGAGTTCT  
E T K T A L L L V R F R R R E Q R T R M R R Y L S C F G C A D Y K L C K V S 360  
120

GCCATATGAAGACATTTGTGAGCTGAGAGACGCTCTGAACTCAAAACAGATGGCGGCTCAATTCAGTAAGTCTTAGAGAGATACCATCAAGTCCGTTGCGAAATACCAG  
A I L K S I G E L R E R S E A I K T D G G S I Q V T C R E I P I K S V V G N T T 480  
160

ATGATGACACAGTTTGGATTTCTCAGTGAAGAGAGAGAAAGAGATCATTTGTTTATGACCTGTTGGGTTGGAGACACACGTTAATGCAGAGCATTAACAACGACTGATC  
M M E Q V L E F L S E E E R G I I G V Y G P G G V G K T T L M Q S I N N E L I 600  
200  
kinase-1a

ACAAAGACATCAGTATGATGATCTGATTTGGGTTCAATGTCAGAGAAATTCGCGAGTGTACAAATTCAGCAAGCCGTTGGAGCACGGTTGGCTTATCTTGGAGCAGAGAGACC  
T K G H Q Y D V L I W V Q M S R E F G E C T I Q Q A V G A R L G L S W D E K E T 720  
240

GGCGAAACAGAGCTTTGAGATATACAGAGCTTTGAGACAGAAACGTTCTGTGTTGTTGCTAGATGATCTTGGAAGAGATAGACTTGGAGAAACTGAGTTCCTCGACCTGACAGG  
G E N R A L K I Y R A L R Q K R F L L L L D D V W E E I D L E K T G V P R P D R 840  
280  
kinase-2

Fig. 6A

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GAACAATGCAAGTGTATTCACGACGCTTATACATTATGCAACATATGCGTGGCAATACAGTTGAGCTGAGTTCTGGAAGAAGAACACCGCTGGAGCTGTCTGT  
E N K C K V M F T T R S I A L C N N M G A E Y K L R V E F L E K K H A W E L F C 320

AGTAAGTATGAGAAAGATCTTTAGAGTCATCATTCGCGCGGAGATTATAGTGAATGTTGAGGATGCCACTAGCCCTTGATCACTTTAGAGGAGCCATGCT  
S K V W R K D L L E S S S I R L A E I I V S K C G G L P L A L I T L G G A M A 1080  
360

kinase-3a

membrane integrated

CATAGAGACAGAGAAGAGTGATCCATGCTAGTGAATCTGACTAGATTCCAGACAGATGAAGGTATGAATATGTTGCCCTTTGAATTCAGCTACGACCACTCGAG  
H R E T E E W I H A S E V L T R F P A E M K G M N Y V F A L L K F S Y D N L E 400  
1200

AGTATCTGCTGCTGCTGTTCTGTAATGCGCTTATCCAGAGAATCTATAGATGAGCAGCTTGTGACTGCGTGGCGAAGGTTTCTCACCAGCTCCATGCG  
S D L L R S C F L Y C A L F P E E H S I E I E Q L V E Y W V G E G F L T S S H G 440  
1320

GTTAACACCATTTACAGGATATTTCTCATTTGGGATCTGAAGCGCATGTTGTGAAACCGGAGATGAGAAACACAGGTGAGATGATATATGTGTCAGAACCTTTGCATTG  
V N T I Y K G Y F L I G D L K A A C L L E T G D E K T Q V K M H N V V R S F A L 480  
1440

TGGATGCCATCTGAACAGGGACTTATTAAGAGCTGATCTAGTTGAGCCATGAGATGGACATACTGAAGCTCCTAAGCAGAAACTGGCACAACCGTTGTTGATCTCATTTGATG  
W M A S E Q G T Y K E L I L V E P S M G H T E A P K A E N W R Q A L V I S L L D 520  
1560

AACAGATCCAGACCTTGCCCTGAATACTCATATGCCGAAACTGACACACTGATGCTCCAAACAGACAGCTTTTGAAGAGATTCCAACAGCGTTTTCATGATATGCCGTCTC  
N R I Q T L P E K L I C P K L T T L M L Q Q N S S L K K I P T G F F M H M P V L 560  
1680

AGAGTCTTGACTGTCTGTCACAGATATCATGAGATTCCTGCTGCTATCAAGATTTGGTGAGTTGTATCATCTGCTATGTCAGGACAAAGATAGTATTTGCCACAGAGCTT  
R V L D L S F T S I T E I P L S I K Y L V E L Y H L S M S G T K I S V L P Q E L 600  
1800

Fig. 6B

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GGGATCTTGAAGAACTGAAGCATCTGACCTACAAAGAACTCAGTTCTTCAGACGATCCACGAGATGCCATATGTTGGCTGAGCAAGCTCGAGGTTCTGAACTTGTAACCTACAGTTAC  
G N L R K L K H L D L Q R T Q F L Q T I P R D A I C W L S K L E V L N L Y Y S Y 640  
GCCGTTGGAACTGCAGAGCTTTGAGAGAGATGAAGCAGAACTCCGATTCCGTGACTTGGAATACCTTGAAAACCTAACACACTCCGTAATCACTGTTCTCTCATTTGAGACCCTA  
A G W E L Q S F G E D E A E E L G E A D L E Y L E N L T T L G I T V L S L E T L 680  
AAACTCTCTTCGAGTTCCGTCCTTTGCATAAACAATATACAGCATCTCCACGTTGAGAGTGCAATGAACTCCCTACTTCAATCTCCATCACTACTAACCATGGCAGAACCTGAGA  
K T L F E F G A L H K H I Q H L H V E E C N E L L Y F N L P S L T N H G R N L R 720  
AGACTTACGATTAAAGTTGCCATGACTTGGAGTACCTGTCACACCCGACAGATTTGAAATGATTGGCTTCGAGTCTAGAGTTCTGACGTTACACAGCCTTCACAACCTTAACCGA  
R L S I K S C H D L E Y L V T P A D F E N D W L P S L E V L T L H S L H N L T R 760  
GTGTGGGAAATTTCTGAAGCCAAGATTGTCTGCGAATATCCGTTGCATTAACATTTACACACTGCAACAAGCTGAAGAATGTCATGGGTTGAGAACTCCCAAGCTAGAGGTGATT  
V W G N S V S Q D C L R N I R C I N I S H C N K L K N V S W V Q K L P K L E V I 800  
GAACCTTCGACTGCAGAGATGAGGAATTCATTAAGCGAAGACGAGAGTCCGTCGAGATCCAAACATTTGTTCCCAAGCCTGAAGACCTTGAGAACTAGGGATCTGCCAGAACTA  
E L F D C R E I E E L I S E H E S P S V E D P T L F P S L K T L R T R D L P E L 840  
AACAGCATCTCCCATCTCGATTTCATTCCAAAAAGTTGAACATTAAGTATCACAATGCCCCAGAGTTAAGAACTGCCGTTTCAGAGAGAGAGACCCAGATGAATGCACTGCCAACA  
N S I L P S R F S F Q K V E T L V I T N C P R V K K L P F Q E R R T Q M N L P T 880

Fig. 6C

GTTTATTTGTGAGAGAAATGCTGGAACCACTGGAATAAGATCAACCAACGAGAGCTTTGTTATTTACCGCGCTTTGTTCCAAATTGATATAAGAGCTAAGAGCACTCTGTACAATA 2760  
V Y C E E K W W K A L E K D Q P N E E L C Y L P R F V P N \* 909

TGTCATTTTCATAGTACGAGAGAGCCAGAGAGTGTCTCAGTGAATCATCACTTCCACTAGACCACAAACTAGAGATTATGTATCATAAACCCTATCCGCGATCAATA 2880

GATCTCAGACTATGAGAGAGAGACTCACCAGTATCGTCGATATAGAACTCCAAGCTCCAGTCCGATCAGTGAAGACGACAGATTATCAGATCTCTGCAACAATTCTGGAATC 3000

GTCACCTCAGATTAGACCTCCAGTAAAGAGTGAAGAAAGCATGACGACGACTGTGAAGATTGAGCTAATGAGCTGAACCCGATCCGGAATTGACAGAACCGGATCGAGAGAGAA 3120

TTTTGCATTTGTGCATCTTTATTTTAAATTGTTACGTTGAGCCCCCAATTAATCATAGATATTGTACTGAAGACCAAAATTTCATGGTGATCAATCAATTGTATTTCGTAATTTCGTAAG 3240

TGTAATAACGAGAAAAGGAATAAAAGGTCACTGAGT (A)<sub>n</sub>

Fig. 6D



consensus

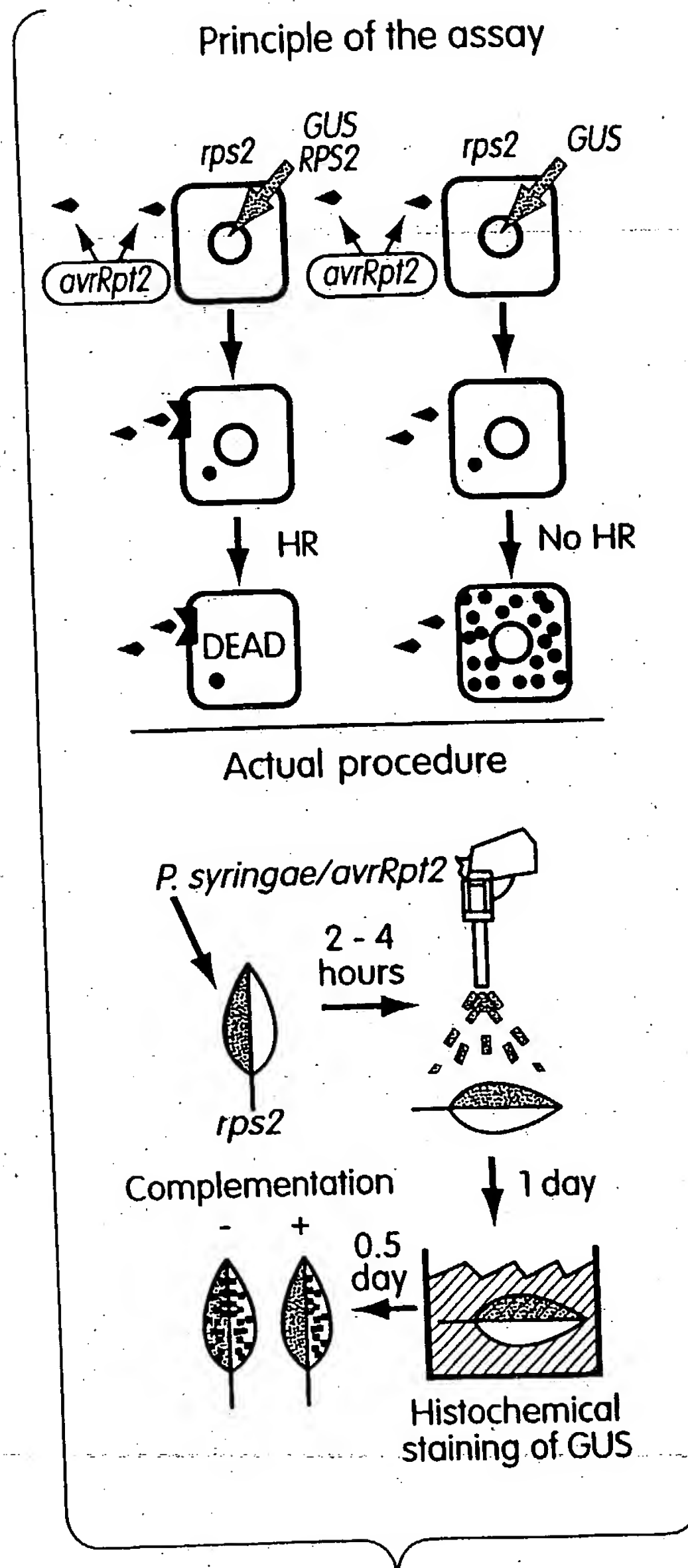
PXXaXX LXXLXXLXaXXXX aXXa

505	PKAENW RQALVISLLD NR IQTL	
527	PEKLIC PK LTTMLQQNSSLKKI	
550	PTGFFMHMPVLRVLDLSFTS ITEI	
574	PLSIKY LVELYHLSMSGTK ISVL	
597	PQELGN LRKLKHLDLQRTQFLQTI	
621	PRDAICWLSKLEVLNLYYSYAGWEL	QSFGEDEAEELG
658	FADLEY LENLTTLGITVLS LETL	KT
683	LFEFGALHKHIQHHLHVEECNELLYF	NL
710	P SLTNHGRNLRRLSIKSCHDLEYL	VT
736	PADFENDWLPSLEVLTLSLHNLTRV	WGN
765	SVSQDC LRNIRCINISHCNKLKNV	SWVQKL
795	PK LEV IELFDCREIEELISEHES	PSVED
823	PT LFPSLKTLRTRDLPELNSI L	
845	PSRFS FQKVETLVITNCPRVKKL	

Fig. 7

Leucine zipper 60  
MDFISSLIYG CAQVLCESMN MAERRGHKTD LRQAITDLET AIGDLKAIRD DLTLRIOQDG 120  
LEGRSCSNRA REWLSAVQVT ETKTALLVR FRRREQRTM RRRYLSCFGC ADYKLCCKVS 180  
ALLSIGELR ERSEAIKTDG GSIQVTCREI PIKSVGNNT MMEQVLEFLS EEEERGIIIGV 240  
P loop  
YGPGGVGKTT LMQSINNELI TKGHQYDVI WVQMSREFGE CTIQAVGAR LGLSWDEKET 300  
GENRALKIYR ALRQKRELL LDDVWEIDL EKTGVRPRDR ENCKVMFTT RSIALCNNMG 360  
AeykIrvEFL EKkHawELFC SKVWRKDLE SSIRRLAEI IVSCKGLPL ALITLGAMA 420  
HRETEEWIH ASEVLTFRPA EMKGMNYFA LKFSYDNLE SDLRSCFLY CALFPEHSI 480  
EIEQLVEYWV GEGFLTSSHG VNTIYKGYFL IGDKAACLL ETGDEKTQVK MHNVRSFAL 540  
WMASEQGYK ELILVEPSMG HTEAPKAENW RQALVISLD NRIQTLPEKL ICPKLTITML 600  
QONSSLIKIP TGFPMMPVL RVLDSFTSI TEIPLSIKYL VELYHLSMSG TKISVLPQEL 660  
GNLRKLKHL D LQRTQFLQTI PRDAICWLSK LEVLNLYSY AGWELQSFGE DEAEELGFAD 720  
LEYLENLTTL GITVLSLETI KTLFFEGALH KHIOHLVEE CNELLYFNLP SLTNHGRNLR 780  
RLSIKSCHDL EYLVTPADFE NDWLPSEVL TLHSLHNLTR VWGNSVSQDC LRNIRICINIS 840  
(end Leucine-rich repeats)  
HCNKLKNVSW VQKLPKLEVI ELFDCREIEE LISEHESPSV EDPTLPSPK TLKTRDLPEL 900  
NSILPSRFSF QKVETLVITN CPRVKKLPFQ ERRTOQNLPT VYCEEKWKKA LEKDQPNNEEL 909  
CYLPRFVFN

Fig. 8



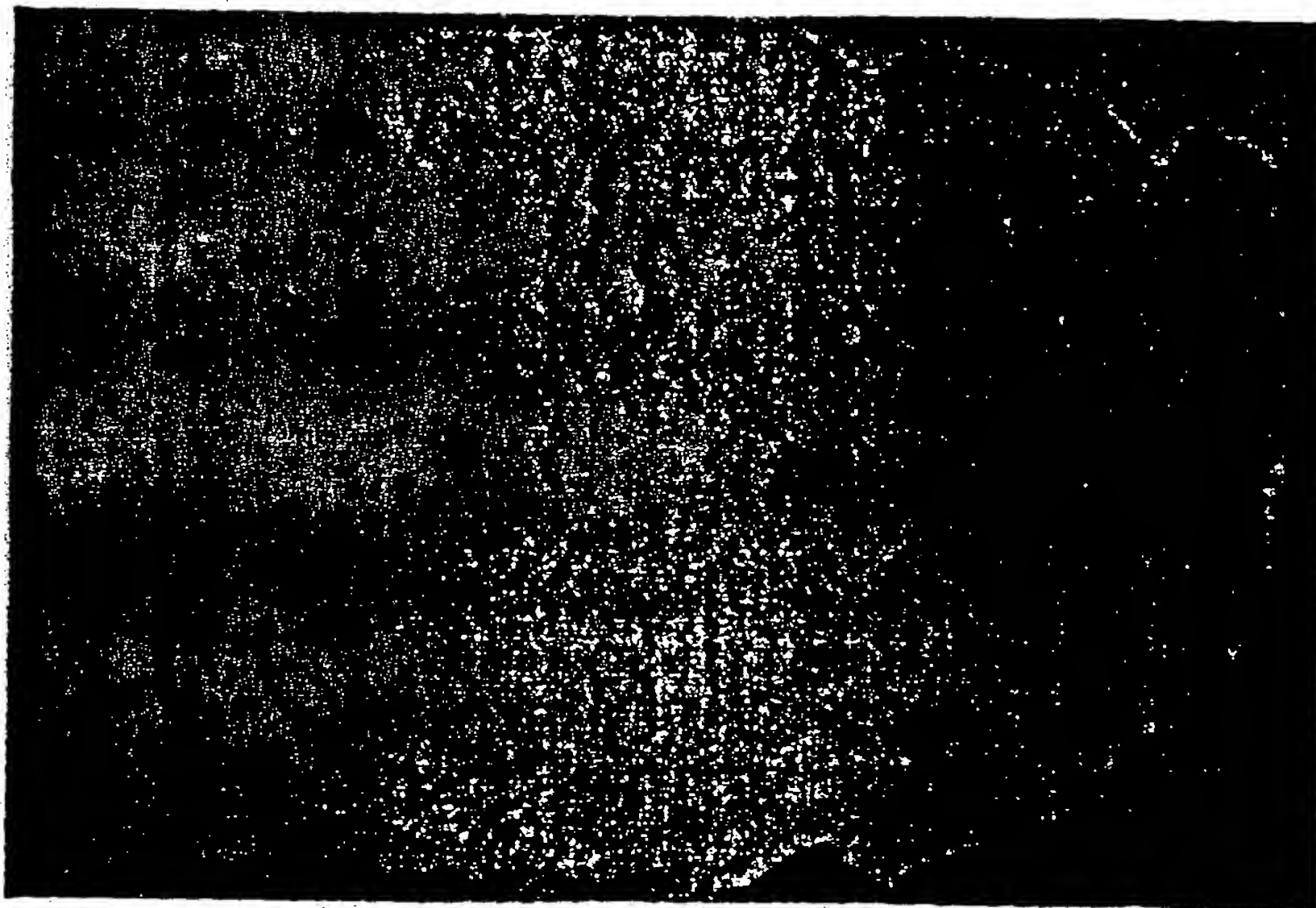


Fig. 10B

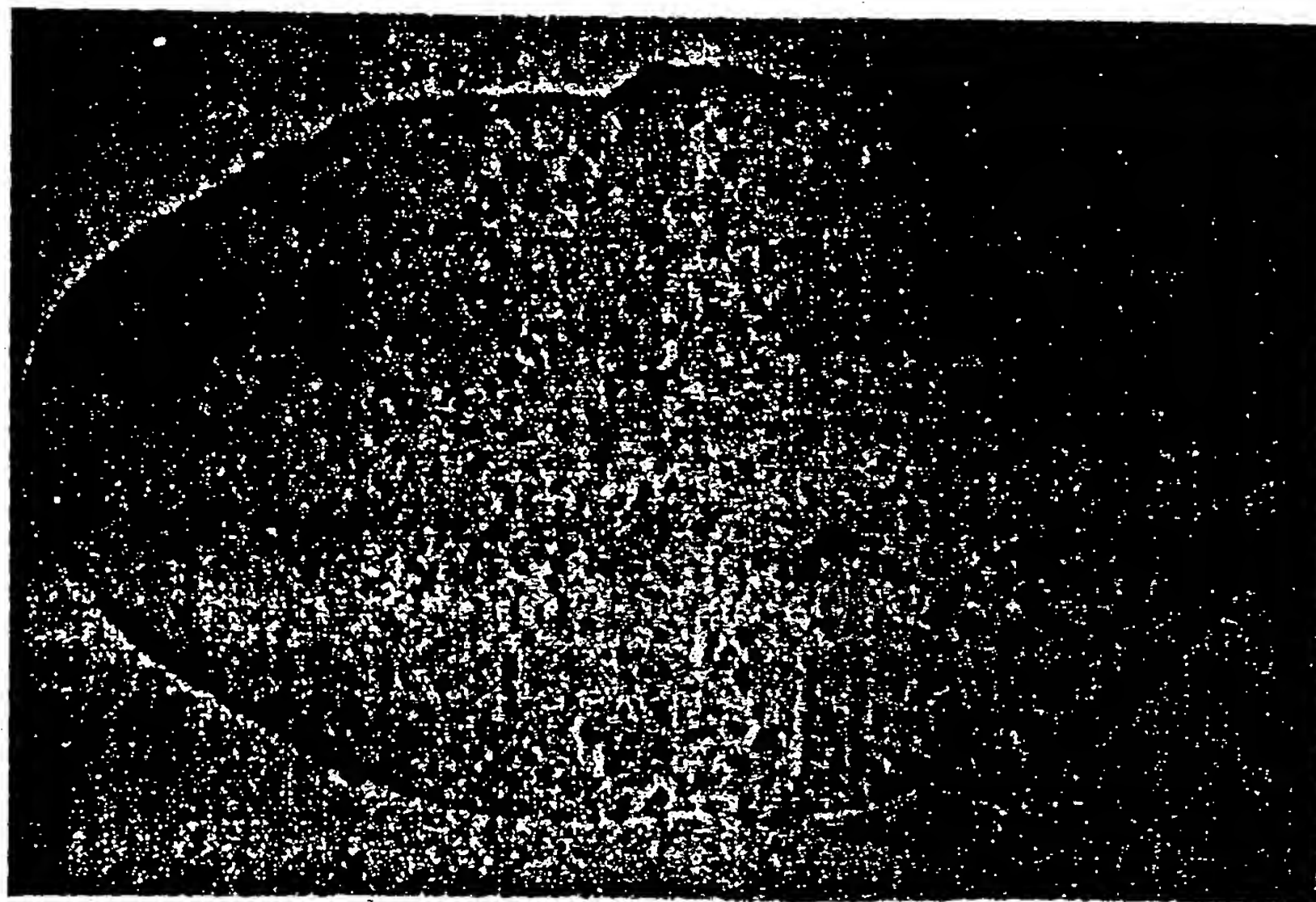


Fig. 10A

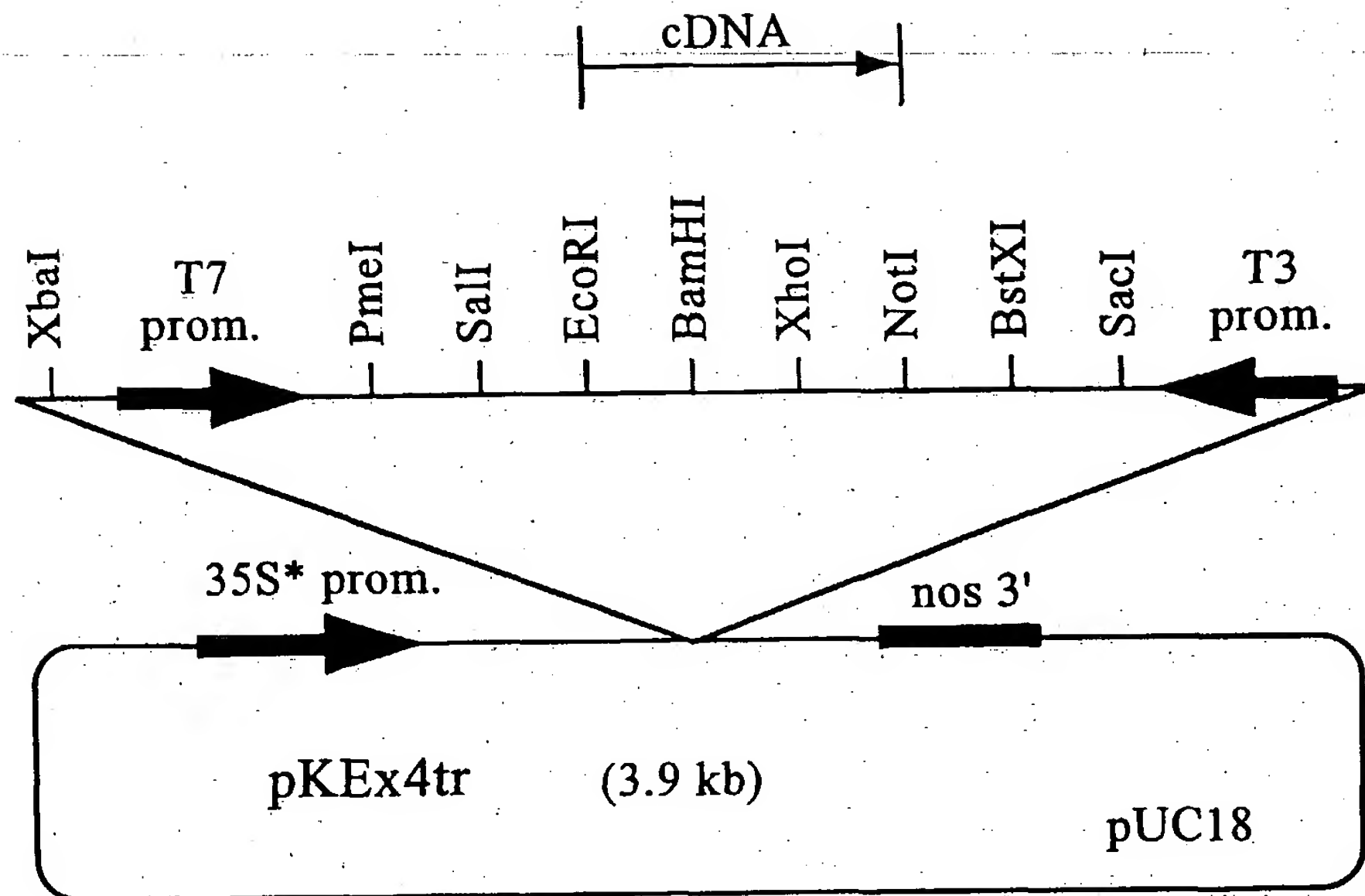


Fig. 11



Title: RPS GENE FAMILY, PRIMERS, PROBES, AND  
DETECTION METHODS

Applicant(s): Ausubel et al.

Filing Date: July 2, 2003

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Customer No.: 21559

	10	20	30	40	50	60	
1	aagctttaca	gattggatga	tctcttaatg	catgctgaag	tgactgcaaa	aaggtagca	60
61	atattcagt	gttctcgta	tgaatatttc	atgaacggaa	gcagcactga	gaaaatgagg	120
121	cccttggtat	ctgattttct	gcaagagatt	gagtctgtca	aggtagagtt	cagaaatggt	180
181	tgcttgcaag	ttctggatat	atcacctttt	tccctgacag	atggagaagg	ccttggttaat	240
241	ttcttattaa	aaaaccaggc	caaggtgccg	aatgatgatg	ctgtttcttc	tgatggaagt	300
301	ttagaggatg	caagcagcac	tgagaaaatg	ggacttccat	ctgattttct	ccgagagatt	360
361	gagtctgttg	agataaagga	ggccagaaaa	ttatatgata	aagttttgga	tgcaacacat	420
421	tgtgagacga	gtaagcacga	tggaaaaagc	tttatcaaca	ttatgttaac	ccaacaggac	480
481	aaggtgctgg	actatgatgc	tggttcagt	tcttatcttc	ttaaccaa	ctcagtagtt	540
541	aaagacaaaa	tattgcacat	tggctcttta	cttgtagata	ttgtacagta	ccggaatatg	600
601	catatagaac	ttacagatct	cgctgaacgt	gttcaagata	aaaactacat	tcgtttcttc	660
661	tctgtcaagg	gttatattcc	tgcttggtat	tacacactat	atctctctga	tgtcaagcaa	720
721	ttgcttaagt	ttgttgaggc	agaggtaaag	attatttgtc	tgaaagtacc	agattcttca	780
781	agttatagct	tccctaagac	aaatggatta	ggatatctca	attgcttttt	aggcaaattg	840
841	gaggagcttt	tacgttctaa	gctcgatttg	ataatcgact	taaaacatca	gattgaatca	900
901	gtcaaggagg	gcttattgtg	cctaagatca	ttcattgatc	atttttcaga	aagctatggt	960
961	gagcatgatg	aagcttgtgg	tcttatagca	agagtttctg	taatggcata	caaggctgag	1020
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1381	tctcgcttcg	atgtccatgc	tcaatgtgtt	gtgactcaat	tatattcatg	gagagagttg	1440
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2221	catggaaaag	gccaaacaag	aggatttcct	tctccagatc	aataggtaaa	aaaaactgta	2280
2281	ttaattttac	attacaaaaa	aaaagaactg	tattaatttt	actgtattat	gtttatgcca	2340
2341	actctcattt	ccatgtgttc	tcttttattc	aattcagttg	agaaggtgta	tttcctgaac	2400
2401	gattggaaga	ataccgattg	ttcgttcatt	cttaccaaga	tgaattgat	ctgtggcgcc	2460
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2521	ggccgcgtga	tatctccttc	atttttgaga	gcttcaagct	tgtaaagt	ttggatttgg	2580

Fig. 12A

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2941	tgagttgcat	attttcaggg	acatttggtt	attcaaggaa	attgaagggt	aggtgtgttc	3000
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Fig. 12B